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TECH CENTER 1600/2300



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Doherty, Joni Kristin, Gail M. Clinton, and John P. Adelman

(ii) TITLE OF INVENTION: HER-2 BINDING ANTAGONISTS

(iii) NUMBER OF SEQUENCES: 9

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: DAVIS WRIGHT TREMAINE LLP
- (B) STREET: 1501 Fourth Avenue, 2600 Century Square
- (C) CITY: Seattle
- (D) STATE: Washington
- (E) COUNTRY: U.S.A.
- (F) ZIP: 98101

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk/
- (B) COMPUTER: PC compatible
- (C) OPERATING SYSTEM: Windows95
- (D) SOFTWARE: Word

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 09/234,208
- (B) FILING DATE: January 20, 1999
- (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Davison, Barry L.
- (B) REGISTRATION NUMBER: P47,309
- (C) REFERENCE/DOCKET NUMBER: 49321-1

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 206 628-7621
- (B) TELEFAX: 206 628-7699

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: HER-2 ECD antagonist

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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Gly	Thr	His	Ser	Leu	Leu	Pro	Arg	Pro	Ala	Ala	Val	Pro	Val	Pro	Leu
				5					10					15	
Arg	Met	Gln	Pro	Gly	Pro	Ala	His	Pro	Val	Leu	Ser	Phe	Leu	Arg	Pro
					20			25					30		
Ser	Trp	Asp	Leu	Val	Ser	Ala	Phe	Tyr	Ser	Leu	Pro	Leu	Ala	Pro	Leu
					35			40					45		
Ser	Pro	Thr	Ser	Val	Pro	Ile	Ser	Pro	Val	Ser	Val	Gly	Arg	Gly	Pro
					50			55				60			
Asp	Pro	Asp	Ala	His	Val	Ala	Val	Asn	Leu	Ser	Arg	Tyr	Glu	Gly	
					65			70				75			

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 419
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: polypeptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	Leu	Ala	Ala	Leu	Cys	Arg	Trp	Gly	Leu	Leu	Leu	Ala	Leu	Leu
					5				10				15		
Pro	Pro	Gly	Ala	Ala	Ser	Thr	Gln	Val	Cys	Thr	Gly	Thr	Asp	Met	Lys
					20			25					30		
Leu	Arg	Leu	Pro	Ala	Ser	Pro	Glu	Thr	His	Leu	Asp	Met	Leu	Arg	His
					35			40				45			
Leu	Tyr	Gln	Gly	Cys	Gln	Val	Val	Gln	Gly	Asn	Leu	Glu	Leu	Thr	Tyr
					50			55				60			
Leu	Pro	Thr	Asn	Ala	Ser	Leu	Ser	Phe	Leu	Gln	Asp	Ile	Gln	Glu	Val
					65			70			75		80		
Gln	Gly	Tyr	Val	Leu	Ile	Ala	His	Asn	Gln	Val	Arg	Gln	Val	Pro	Leu
					85				90				95		
Gln	Arg	Leu	Arg	Ile	Val	Arg	Gly	Thr	Gln	Leu	Phe	Glu	Asp	Asn	Tyr
					100				105				110		
Ala	Leu	Ala	Val	Leu	Asp	Asn	Gly	Asp	Pro	Leu	Asn	Asn	Thr	Thr	Pro
					115				120				125		
Val	Thr	Gly	Ala	Ser	Pro	Gly	Gly	Leu	Arg	Glu	Leu	Gln	Leu	Arg	Ser
					130			135				140			
Leu	Thr	Glu	Ile	Leu	Lys	Gly	Gly	Val	Leu	Ile	Gln	Arg	Asn	Pro	Gln
					145			150				155			160
Leu	Cys	Tyr	Gln	Asp	Thr	Ile	Leu	Trp	Lys	Asp	Ile	Phe	His	Lys	Asn
					165				170				175		
Asn	Gln	Leu	Ala	Leu	Thr	Leu	Ile	Asp	Thr	Asn	Arg	Ser	Arg	Ala	Cys
					180				185				190		
His	Pro	Cys	Ser	Pro	Met	Cys	Lys	Gly	Ser	Arg	Cys	Trp	Gly	Glu	Ser

195	200	205													
Ser	Glu	Asp	Cys	Gln	Ser	Leu	Thr	Arg	Thr	Val	Cys	Ala	Gly	Gly	Cys
210						215					220				
Ala	Arg	Cys	Lys	Gly	Pro	Leu	Pro	Thr	Asp	Cys	Cys	His	Glu	Gln	Cys
225						230				235			240		
Ala	Ala	Gly	Cys	Thr	Gly	Pro	Lys	His	Ser	Asp	Cys	Leu	Ala	Cys	Leu
				245					250				255		
His	Phe	Asn	His	Ser	Gly	Ile	Cys	Glu	Leu	His	Cys	Pro	Ala	Leu	Val
	260						265			270					
Thr	Tyr	Asn	Thr	Asp	Thr	Phe	Glu	Ser	Met	Pro	Asn	Pro	Glu	Gly	Arg
	275					280			285						
Tyr	Thr	Phe	Gly	Ala	Ser	Cys	Val	Thr	Ala	Cys	Pro	Tyr	Asn	Tyr	Leu
	290					295			300						
Ser	Thr	Asp	Val	Gly	Ser	Cys	Thr	Leu	Val	Cys	Pro	Tyr	Asn	Tyr	Leu
305					310				315			320			
Glu	Val	Thr	Ala	Glu	Asp	Gly	Thr	Gln	Arg	Cys	Glu	Lys	Cys	Ser	Lys
				325				330			335				
Pro	Cys	Ala	Arg	Gly	Thr	His	Ser	Leu	Leu	Pro	Arg	Pro	Ala	Ala	Val
	340						345			350					
Pro	Val	Pro	Leu	Arg	Met	Gln	Pro	Gly	Pro	Ala	His	Pro	Val	Leu	Ser
	355						360			365					
Phe	Leu	Arg	Pro	Ser	Trp	Asp	Leu	Val	Ser	Ala	Phe	Tyr	Ser	Leu	Pro
	370					375			380						
Leu	Ala	Pro	Leu	Ser	Pro	Thr	Ser	Val	Pro	Ile	Ser	Pro	Val	Ser	Val
385					390			395			400				
Gly	Arg	Gly	Pro	Asp	Pro	Asp	Ala	His	Val	Ala	Val	Asn	Leu	Ser	Arg
			405						410			415			
Tyr	Glu	Gly													

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGAGCACCAT GGAGCTGGC 19

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

- (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TCCGGCAGAA ATGCCAGGCT CC 22

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AACACAGCGG TGTGAGAAGT GC 22

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATACCGGGAC AGGTCAACAG C 21

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TCTGGGTACC CACTCACTGC 20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 22
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTCACACTGG CACGTCCAGA CC 22

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCACGGATCC ATAGCAGACT GAGGAGG 27